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**MEGABLAST 1.2.3-Paracel [2001-11-20]****Reference:**

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000),  
"A greedy algorithm for aligning DNA sequences",  
J Comput Biol 2000; 7(1-2):203-14.

**Database:** Homo\_sapiens.latestgp.masked.fa  
44,521 sequences; 200,768,834,160 total letters

**Query=** hMSC\_6  
(573 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AC121158.1.1.192160	<u>502</u>	e-139
AC107051.4.1.57025	<u>502</u>	e-139
AC096743.3.1.103765	<u>337</u>	4e-90
AC112249.4.1.146551	<u>311</u>	3e-82

>AC121158.1.1.192160  
Length = 192160

Score = 502 bits (253), Expect = e-139  
Identities = 253/253 (100%)  
Strand = Plus / Plus

Query: 321 cagcctctccccaccggtcactggttagcctcgagtttgaccctcaacatccccagaggat 380  
|||||  
Sbjct: 65034 cagcctctccccaccggtcactggttagcctcgagtttgaccctcaacatccccagaggat 65093

Query: 381 gcctcctaggactcgaacctcatttagtggtctctactgctgatggacgccatgagtgagg 440  
|||||  
Sbjct: 65094 gcctcctaggactcgaacctcatttagtggtctctactgctgatggacgccatgagtgagg 65153

Query: 441 ctgtcgaccaccttgggtgaagtgggtggtctccacgtcccacctgggcagcacgatggcc 500  
|||||  
Sbjct: 65154 ctgtcgaccaccttgggtgaagtgggtggtctccacgtcccacctgggcagcacgatggcc 65213

Query: 501 acagaaaggttgatatctacccccaccagcacaacacatgcagaaatttcaaaagagccta 560  
|||||  
Sbjct: 65214 acagaaaggttgatatctacccccaccagcacaacacatgcagaaatttcaaaagagccta 65273

Query: 561 ttttaagtagatga 573  
|||||  
Sbjct: 65274 ttttaagtagatga 65286

>AC107051.4.1.57025  
Length = 57025

Score = 502 bits (253), Expect = e-139  
Identities = 253/253 (100%)  
Strand = Plus / Plus

Query: 321 cagcctctccccaccggtcactgttagcctcgagtttgaccctcaacatccccagaggat 380  
|||||  
Sbjct: 2903 cagcctctccccaccggtcactgttagcctcgagtttgaccctcaacatccccagaggat 2962

Query: 381 gcctcctaggactcgaacctcatttagtgtctctactgctgatggacgccatgagtggag 440  
|||||  
Sbjct: 2963 gcctcctaggactcgaacctcatttagtgtctctactgctgatggacgccatgagtggag 3022

Query: 441 ctgtcgaccaccttgggtgaagtgggtgtccacgtcccacctgggcagcacgatggcc 500  
|||||  
Sbjct: 3023 ctgtcgaccaccttgggtgaagtgggtgtccacgtcccacctgggcagcacgatggcc 3082

Query: 501 acagaaaggttgatatctacccacccagcacaacacatgcagaaatttcaaaagagccta 560  
|||||  
Sbjct: 3083 acagaaaggttgatatctacccacccagcacaacacatgcagaaatttcaaaagagccta 3142

Query: 561 tttaagtagatga 573  
|||||  
Sbjct: 3143 tttaagtagatga 3155

>AC096743.3.1.103765  
Length = 103765

Score = 337 bits (170), Expect = 4e-90  
Identities = 170/170 (100%)  
Strand = Plus / Plus

Query: 1 atgatgaggaccactgaagacttcacaagcctagtgccacattaaactctaacacggcc 60  
|||||  
Sbjct: 48822 atgatgaggaccactgaagacttcacaagcctagtgccacattaaactctaacacggcc 48881

Query: 61 accaaggggaaggtacatttatctggaggcattcctggagggaggagctccctgggggtttt 120  
|||||  
Sbjct: 48882 accaaggggaaggtacatttatctggaggcattcctggagggaggagctccctgggggtttt 48941

Query: 121 actctaaaggtggcctggagcacggagaaccattaatcatctctaaggt 170  
|||||  
Sbjct: 48942 actctaaaggtggcctggagcacggagaaccattaatcatctctaaggt 48991

>AC112249.4.1.146551  
Length = 146551

Score = 311 bits (157), Expect = 3e-82

Identities = 157/157 (100%)

Strand = Plus / Plus

Query: 167 aggtcgaagaagggggcgaagcagacaccctgagctccaaactgcaggctggggatgagg 226  
|||||  
Sbjct: 66611 aggtcgaagaagggggcgaagcagacaccctgagctccaaactgcaggctggggatgagg 66670

Query: 227 ttgtgcacatcaatgaggtgactctgagcagctccagaaaggaggcagtttccctggtga 286  
|||||  
Sbjct: 66671 ttgtgcacatcaatgaggtgactctgagcagctccagaaaggaggcagtttccctggtga 66730

Query: 287 aaggatcctacaagaccctcaggctggtagtgcgag 323  
|||||  
Sbjct: 66731 aaggatcctacaagaccctcaggctggtagtgcgag 66767

Database: Homo\_sapiens.latestgp.masked.fa  
Posted date: Jan 4, 2003 2:12 PM  
Number of letters in database: 200,768,834,160  
Number of sequences in database: 44,521

Lambda K H  
1.37 0.711 1.31

Gapped  
Lambda K H  
1.37 0.711 1.31

Matrix: blastn matrix:1 -3  
Gap Penalties: Existence: 0, Extension: 0  
Number of Hits to DB: 0  
length of query: 1148  
length of database: 200,768,834,160  
effective HSP length: 21  
effective length of query: 552  
effective search space used: 0  
T: 0  
A: 0  
X1: 0 ( 0.0 bits)  
X2: 20 (39.6 bits)  
S1: 12 (24.3 bits)  
S2: 38 (75.8 bits)